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Figure 1

M K H L W F F L L L V A A P R  
GAC ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA

+1 10  
W V L S Q V Q L Q E A G P G L V  
TGG GTC TTG TCC CAG GTG CAG CTG CAG GAG GCG GGC CCA GGA CTG GTG

20  
K P S E T L S L T C S V S G G S  
AAG CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC

30 40  
I S G D Y Y W F W I R Q S P G K  
ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG

50 60  
G L E W I G Y I Y G S G G G T N  
GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT

70  
Y N P S L N N R V S I S I D T S  
TAC AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC

80 90  
K N L F S L K L R S V T A A D T  
AAG AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG

100  
A V Y Y C A S N I L K Y L H W L  
GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA

110 120  
L Y W G Q G V L V T S S  
TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC



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Figure 2

M A W A L L L L G L L A H F T  
ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA

+1 10  
D S A A S Y E L S Q P R S V S V  
GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG

20  
S P G Q T A G F T C G G D N V G  
TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA

30 40  
R K S V Q W Y Q Q K P P Q A P V  
AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG

50 60  
L V I Y A D S E R P S G I P A R  
CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA

70  
F S G S N S G N T A T L T I S G  
TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG

80 90  
V E A G D E A D Y Y C Q V W D S  
GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT

100  
T A D H W V F G G G T R L T V L  
ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA

109  
G  
GGT



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Figure 3

Frame 1 Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp Ser Ala Ala  
ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA GAC TCT GCG GCC  
9 18 27 36 45 54

Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser Pro Gly Gln Thr Ala Gly Phe Thr  
TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG TCC CCA GGA CAG ACG GCC GGG TTC ACC  
66 75 84 93 102 111 120

Cys Gly Gly Asp Asn Val Gly Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala  
TGT GGG GGA GAC AAC GTT GGA AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC  
129 138 147 156 165 174 183

Pro Val Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe Ser Gly  
CCT GTG CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA TTC TCT GGC  
192 201 210 219 228 237 246

Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val Glu Ala Gly Asp Glu Ala Asp  
TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG GTC GAG GCC GGG GAT GAG GCT GAC  
255 264 273 282 291 300 309

Tyr Tyr Cys Gln Val Trp Asp Ser Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu  
TAT TAC TGT CAG GTG TGG GAC AGT ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CCG CTG  
318 327 336 345 354 363 372

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu  
ACC GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT GAG GAG  
381 390 399 408 417 426 435

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr  
CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC TTC TAC CCG GGA GCC GTG ACA  
444 453 462 471 480 489 498

Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys  
GTG GCC TGG AAG GCA GAT AGC AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA  
507 516 525 534 543 552 561

Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
CAA AGC AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG TCC  
570 579 588 597 606 615 624

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro  
CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG GAG AAG ACA GTG GCC CCT  
633 642 651 660 669 678 687

Thr Glu Cys Ser TER  
ACA GAA TGT TCA TGA



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INVENTOR: Nabii HANNA et al.  
FILED: July 10, 2000  
ATTORNEY DOCKET: 037003/0275543  
IDEC REF. NO.: 1999-30-0019CP4C1  
TITLE: RECOMBINANT ANTI-CD4 ANTIBODIES OR HUMAN THERAPY  
PILLSBURY WINTHROP LLP  
MCLEAN, VIRGINIA

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Figure 4a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC TTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGC  
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Ser Glu Ser Thr Ala Ala Leu Gly  
CCA TCC GTC TTC CCC CTG GCG CCC TCC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC  
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC  
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro



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## Figure 4b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA	696	705	714	723	732	741	750
Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	GCA CCT GAG TTC CTG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC	759	768	777	786	795	804
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu	ATG ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG GAA GAC CCC GAG	822	831	840	849	858	867
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG	885	894	903	912	921	930
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu	GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG	948	957	966	975	984	993
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr	AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC	1011	1020	1029	1038	1047	1056
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu	ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG TAC ACC CTG CCC CCA TCC CAG GAG	1074	1083	1092	1101	1110	1119
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile	GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC	1137	1146	1155	1164	1173	1182
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu	GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG	1200	1209	1218	1227	1236	1245
Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu	GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG	1263	1272	1281	1290	1299	1308
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	GGG AAT GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC	1326	1335	1344	1353	1362	1371
Leu Ser Leu Ser Leu Gly Lys TER	CTC TCC CTG TCT CTG GGT AAA TGA	1389	1398				



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# Figure 5a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC  
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC  
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

**PILLSBURY WINTHROP LLP**  
**MCLEAN, VIRGINIA**

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### Figure 5 b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA TCA TGC CCA  
696 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC  
759 768 777 786 795 804 813

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840			849			858			867			876

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903			912			921			930			939

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu  
GAG CAG TTC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC GAG GAC TGG CTG  
948 957 966 975 984 993 1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr  
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC  
1011 1020 1029 1038 1047 1056 1065

Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTC	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG
	1074			1083				1092			1101			1110			1119			1128

Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile		
GAG	ATG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	TTC	TAC	CCC	AGC	GAC	ATC		
			1137			1146			1155			1164			1173			1182			1191	

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG  
1200 1209 1218 1227 1236 1245 1254

Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
GAC	TCC	GAC	GGC	TCC	TTC	TTC	CTC	TAC	AGC	AGG	CTA	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	GAG
		1263			1272			1281			1290			1299			1308			1317

Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	AGC
		1326			1335			1344			1353			1362			1371			1380

Leu Ser Leu Ser Leu Gly Lys TER  
CTC TCC CTG TCT CTG GGT AAA TGA  
1389 1398



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## Figure 6a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
381 390 399 408 417 426 435

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly  
CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG AGC ACA GCC GCC CTG GGC  
444 453 462 471 480 489 498

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC  
507 516 525 534 543 552 561

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG  
570 579 588 597 606 615 624

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro  
GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC GTA GAT CAC AAG CCC  
633 642 651 660 669 678 687

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro



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### Figure 6 b

AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC AAA TAT GGT CCC CCA TGC CCA CCA TGC CCA  
696 705 714 723 732 741 750

Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
GCA CCT GAG TTC GAG GGG GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC  
759 768 777 786 795 804 813

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACG	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAG	GAA	GAC	CCC	GAG
		822			831			840			849			858			867			876

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
GTC	CAG	TTC	AAC	TGG	TAC	GTG	GAT	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG
		885			894			903		912				921			930			939

Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
GAG	CAG	TTC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG	GAC	TGG	CTG
		948			957			966			975			984			993			1002

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr  
AAC GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC GAG AAA ACC  
1011 1020 1029 1038 1047 1056 1065

Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu
ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC	CGA	GAG	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CAG	GAG
	1074			1083				1092			1101			1110			1119			1128

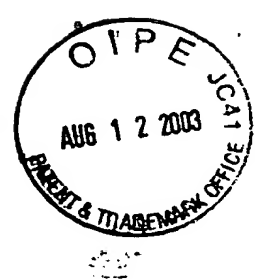
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
GAG ATG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC  
1137 1146 1155 1164 1173 1182 1191

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG  
1200 1209 1218 1227 1236 1245 1254

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu  
 GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG GAC AAG AGC AGG TGG CAG GAG  
 1263 1272 1281 1290 1299 1308 1317

Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
GGG	AAT	GTG	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	TAC	ACA	CAG	AAG	AGC
	1326			1335				1344			1353			1362			1371			1380

Leu Ser Leu Ser Leu Gly Lys TER  
CTC TCC CTG TCT CTG GGT AAA TGA  
1389 1398



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## Figure 7a

### Primers for the Amplification of Monkey Immunoglobulin Heavy Chain Variable Regions

#### 5' 'Sense' Primers

#### A. Human or Monkey heavy chain early leader sequence primers with *Sall* site

- V<sub>H</sub>1 5' ACTAAGTCGACAT GGA CTGGACCTGG 3'
- V<sub>H</sub>2 5' ACTAAGTCGACAT GGACATACTTTGTTCCAC 3'
- V<sub>H</sub>3 5' ACTAAGTCGACAT GGAGTTTGGGCTGAGC 3'
- V<sub>H</sub>4 5' ACTAAGTCGACAT GAAACACCTGTGGTTCTT 3'
- V<sub>H</sub>5 5' ACTAAGTCGACAT GGGGTCAACCGCCATCCT 3'
- V<sub>H</sub>6 5' ACTAAGTCGACAT GTCTGTCTCCTTCCTCAT 3'

#### B. Human or Monkey heavy chain late leader sequence primers with *Mlu* I site

- V<sub>H</sub>1 5' G GCA GCA GC(CT) ACG CGT GCC CAC TCC GAG GT 3' <sup>+1</sup>
- V<sub>H</sub>2 5' G ACC GTC CCG ACG CGT GT(TC) TTG TCC CAG GT 3' <sup>+1</sup>
- V<sub>H</sub>3 5' GCT ATT TTC ACG CGT GTC CAG TGT GAG 3' <sup>+1</sup>
- V<sub>H</sub>4 5' GCG GCT CCC ACG CGT GTC CTG TCC CAG 3' <sup>+1</sup>
- V<sub>H</sub>5 5' G GCT GTT CTC ACG CGT GTC TGT GCC GAG GT 3' <sup>+1</sup>



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## Figure 7b

### C. Human or Monkey framework 1 sequence primers with *Xho* I site

V <sub>H</sub> 1,3a,5	<sup>+1</sup> CAGGTGCAGCTGCTCGAGTCTGG
V <sub>H</sub> 2	<sup>+1</sup> CAGGTCAACTTACTCGAGTCTGG
V <sub>H</sub> 3b	<sup>+1</sup> GAGGTGCAGCTGCTCGAGTCTGG
V <sub>H</sub> 4	<sup>+1</sup> CAGGTGCAGCTGCTCGAGTCGGG
V <sub>H</sub> 6	<sup>+1</sup> CAGGTACAGCTGCTCGAGTCAGG

### 3' 'Anti-Sense' Primers.

### A. Human or Monkey Heavy Chain Constant Region Primers Anti-Sense Strand with *Nhe* I site

IgG <sub>1-4</sub>	<sup>+118</sup> 5' GGC GGA TGC <u>GCT AGC</u> TGA GGA GAC GG 3'	<sup>+110</sup>
	Nhe I	



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## Figure 7c

### Primers for the Amplification of Monkey Immunoglobulin Light Chain Variable Regions

#### 5' 'Sense' Primers

##### A. Human or Monkey kappa light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGTGTTCAGACCCAGGTC 3'
2. 5' ATCACAGATCTCTCACCATGG(GA)G(AT)CCCC(TA)GC(TG)CAGCT 3'
3. 5' ATCACAGATCTCTCACCATGGACATGAGGGTCCCCGCTCAG 3'
4. 5' ATCACAGATCTCTCACCATGGACAC(GAC)AGGGCCCCCACTCAG 3'

##### B. Human or Monkey lambda light chain early leader primers with Bgl II site

1. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCTGCTGCTCC 3'
2. 5' ATCACAGATCTCTCACCATGGCCTGGGCTCCACTACTTC 3'
3. 5' ATCACAGATCTCTCACCATGACCTGCTCCCCTCTCCTCC 3'
4. 5' ATCACAGATCTCTCACCATGGCCTGGACTCCTCTCTTTC 3'
5. 5' ATCACAGATCTCTCACCATGACTTGGACCCCACTCCTC 3'

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### Figure 7d

### 3' 'Anti-Sense' Primers

A. Human or Monkey kappa light chain constant region primer anti-sense strand with *Kon 1* and *BsiW1* sites.

**C<sub>kappa</sub>** <sup>+108</sup> 5' CCG TTT GAT TTC CAG CTT GGT ACC TCC ACC GAA CGT 3' <sup>+97</sup>  
Kpn 1  
<sup>+112</sup> 5' TGC AGC ATC CGT ACG TTT GAT TTC CAG CTT 3' <sup>+103</sup>  
BsiW1

B. Human or Monkey lambda light chain constant region primer anti-sense strand with *Kpn* I, *Hind* III and *Avr* II sites.

**C<sub>Lambda</sub>**

+107 +99  
5' ACC TAG GAC GGT AAG CTT GGT ACC TCC GCC 3'  
Hind III Kpn I

+107 +97  
5' ACC TAG GAC GGT CA(C/G) (C/G)TT GGT ACC TCC GCC GAA CAC 3'  
Kpn I

+110 +102  
5' CTT GGG CTG ACC TAG GAC GGT CAG CCG 3'  
Avr II



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## Figure 8

### A. Heavy Chain Variable Region:

VH1	5'	CCATGGACTGGACCTGG	3'
VH2	5'	ATGGACATACTTTGTTCCAC	3'
VH3	5'	CCATGGAGTTTGGGCTGAGC	3'
VH4	5'	ATGAAACACCTGTGGTTCTT	3'
VH5	5'	ATGGGGTCAACCGCCATCCT	3'
VH6	5'	ATGTCTGTCTCCTTCCTCAT	3'

### B. Heavy Chain Constant Region Anti-Sense Strand:

IgM	5'	<sup>+119</sup> T TGG GGC GGA TGC ACT	<sup>+115</sup> 3'
IgG <sub>1-4</sub>	5'	<sup>+119</sup> GA TGG GCC CTT GGT GGA	<sup>+115</sup> 3'

### C. Light Chain Variable Region:

Kappa	5'	<sup>+4</sup> G ATG ACC CAG TCT CCA (G/T)CC TC	<sup>+10</sup> 3'
Lambda	5'	<sup>-9</sup> CTC A(C/T)T (T/C)(G/A)C TGC (A/C)CA GGG TCC	<sup>-3</sup> 3'

### D. Light Chain Constant Region Anti-Sense Strands:

Kappa	5'	<sup>+115</sup> AA GAC AGA TGG TGC AGC CA	<sup>+110</sup> 3'
Lambda	5'	<sup>+118</sup> G GAA CAG AGT GAC CGA GGG G	<sup>+112</sup> 3'



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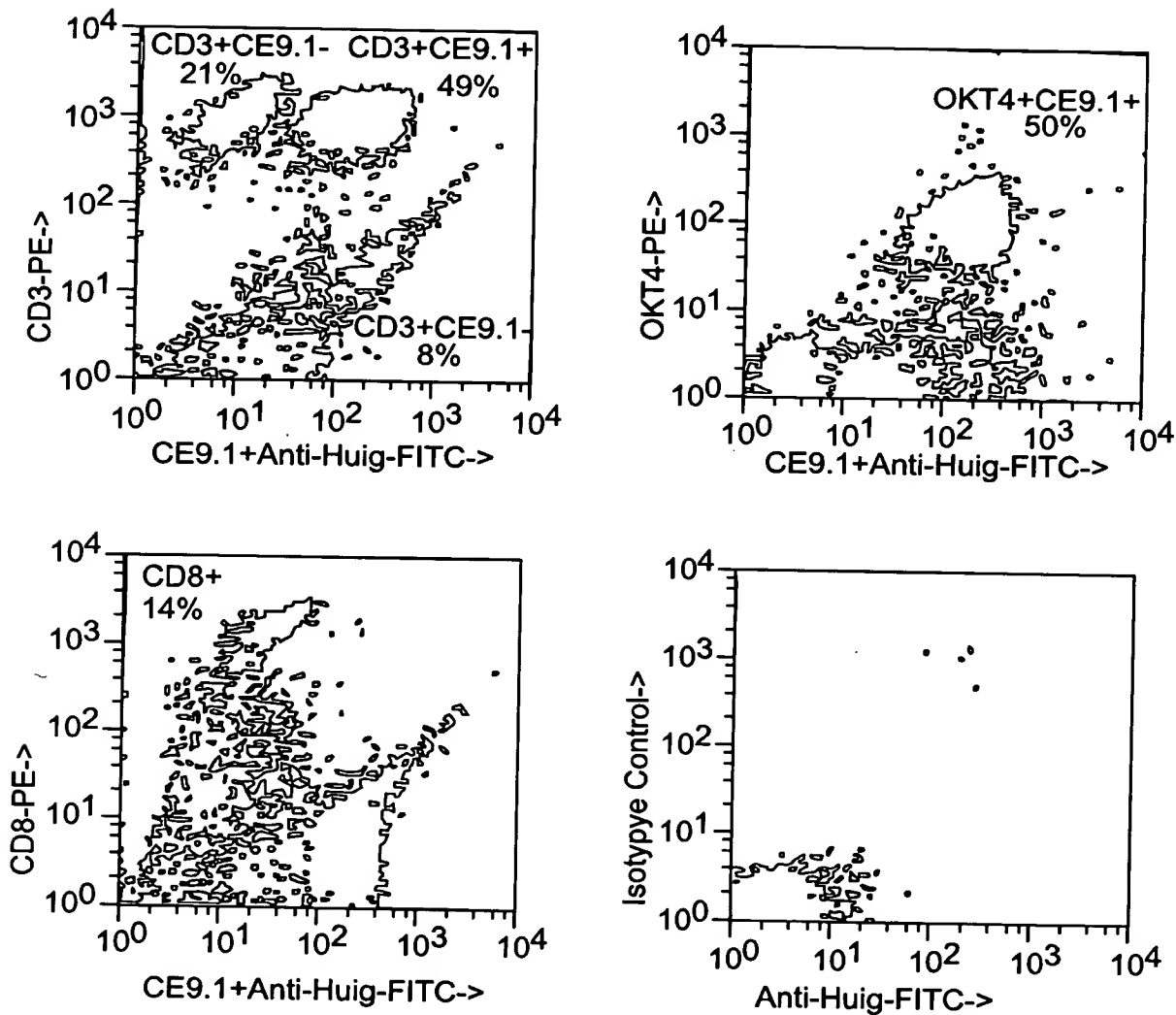


Figure 9



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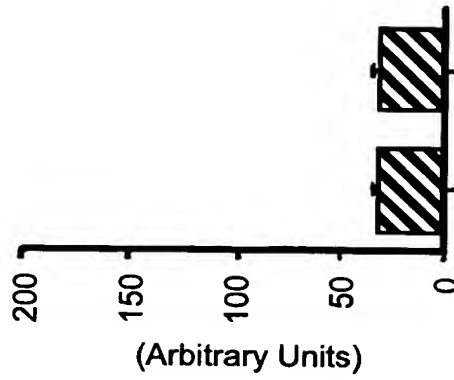


Figure 10c

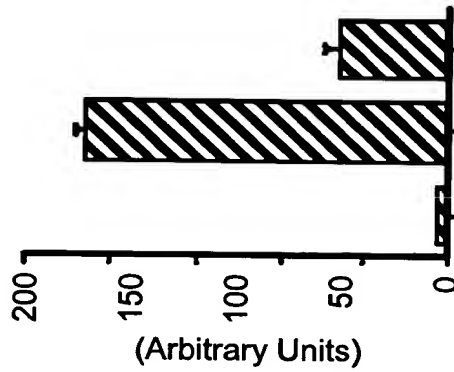


Figure 10b

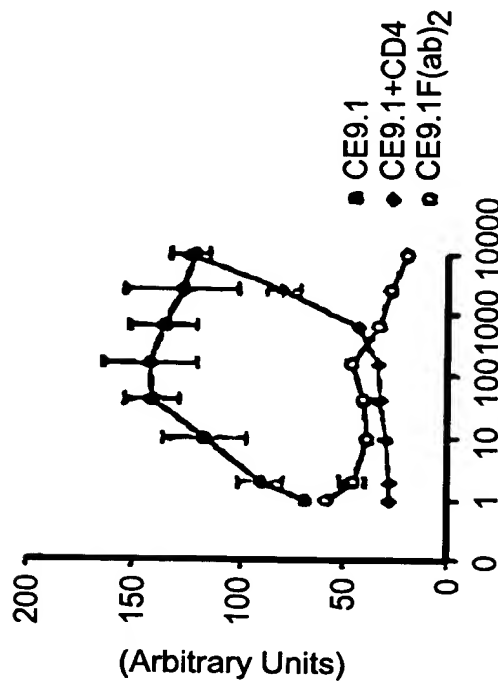


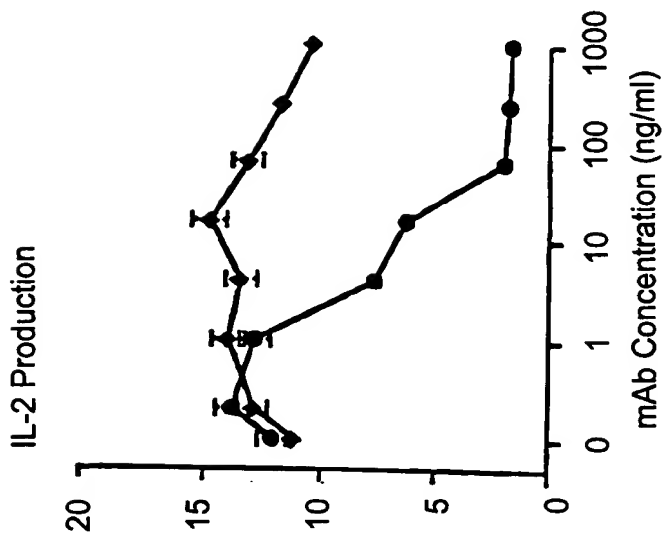
Figure 10a



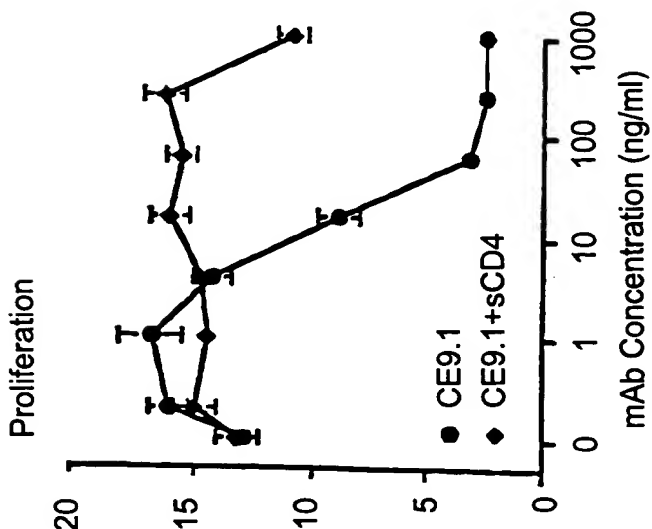


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IL-2 Production  
<sup>3</sup>H-TdR Incorporation by CT20  
(x10<sup>-3</sup> cpm)



<sup>3</sup>H-TdR Incorporation (x10<sup>-3</sup> cpm)

Figure 11



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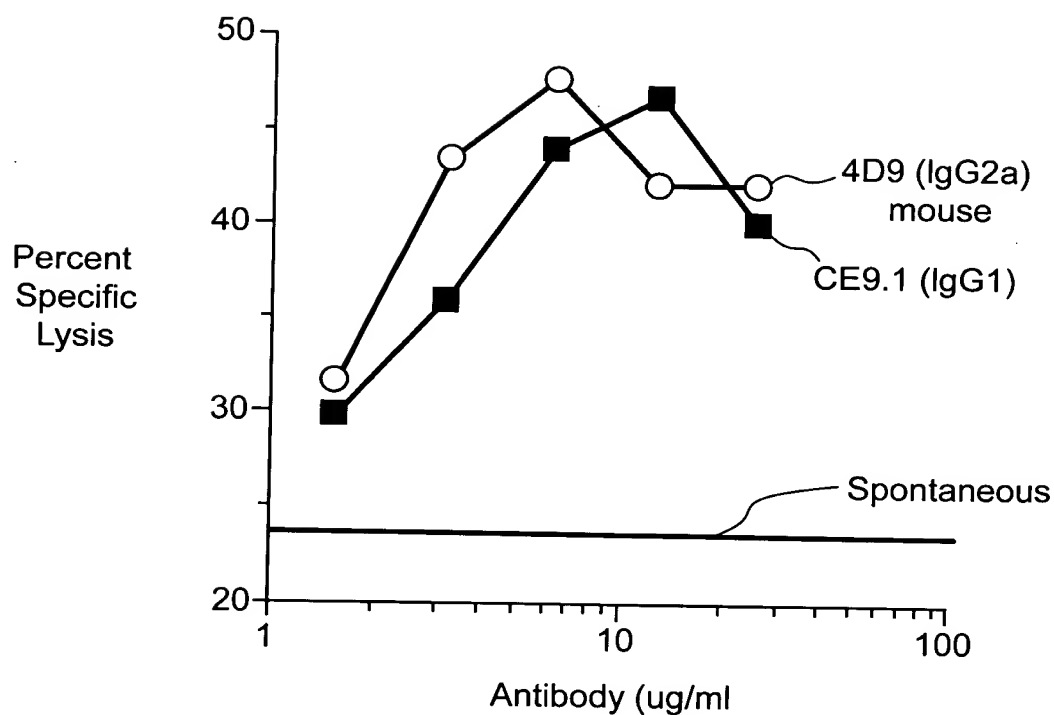


Figure 12



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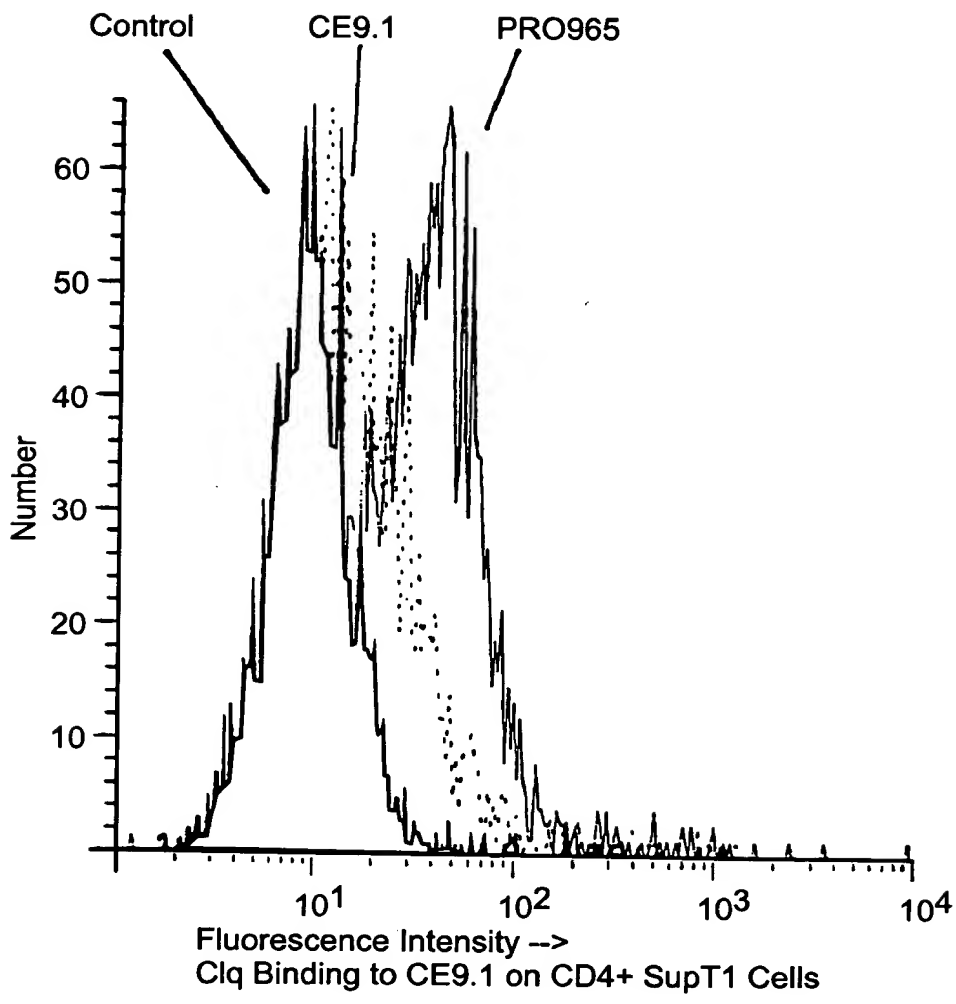


Figure 13



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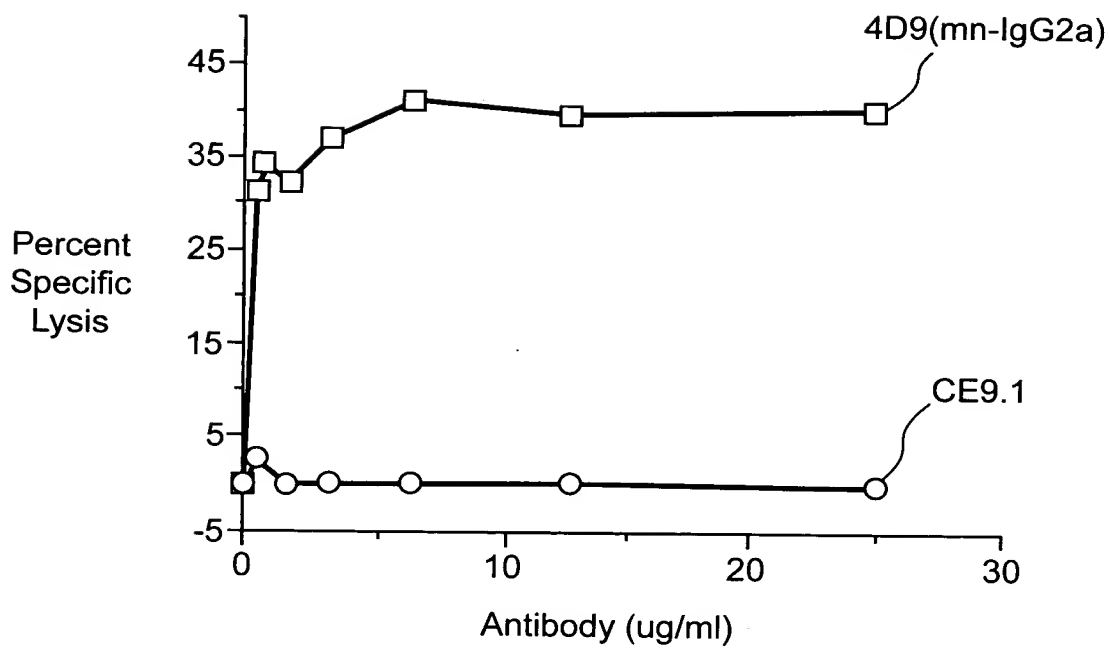


Figure 14



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CD4 and CD8 Cell Counts in Chimpanzees Repeatedly Treated with 10 mpk of CE9.1

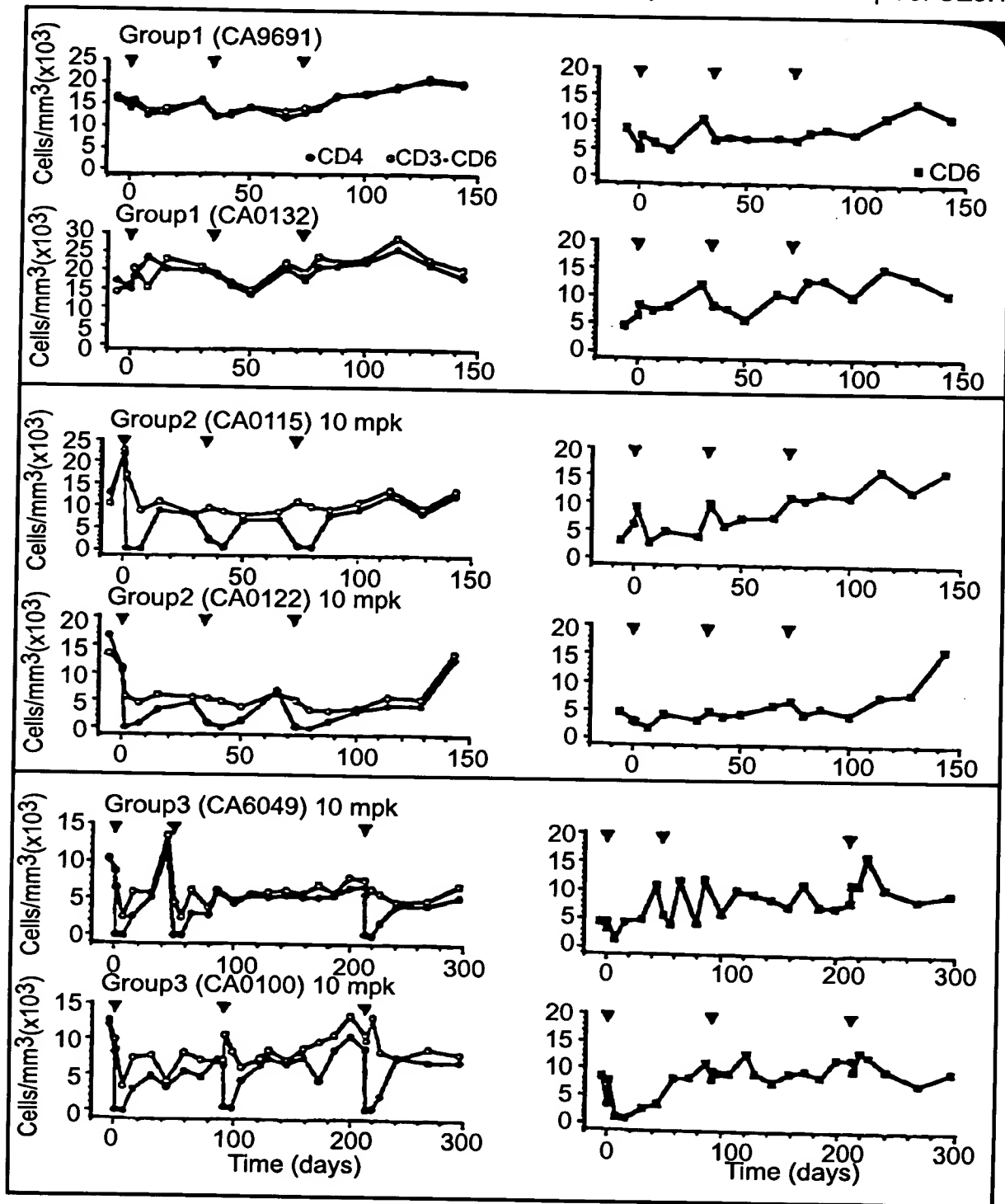


Figure 15



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Figure 16

PCR Primers for Human  $\gamma 4$  Constant Region

1) IDEC 462 3' PCR Primer  
5' GGGG GGA TCC TCA TTT ACC CAG AGA CAG GG 3'  
BamH I

2) IDEC 479 5' PCR Primer  
5' GGGG GCT AGC ACC AAG GGC CCA TCC GTC TTC 3'  
Nhe I

PCR Mutagenesis of Human  $\gamma 4$

3) IDEC 698 3' PCR Primer  
5' CCG GGA GAT CAT GAG AGT GTC CTT GGG TTT TGG GGG GAA CAG GAA GAC  
BspH I

Glu Pro  
TGA TGG TCC CCC CTC GAA CTC AGG TGC TGG GCA TGG TGG GCA TGG GGG 3'

4) Midland GE212 5' PCR Primer

Nhe I  
5' TCC TCA GCT AGC ACC AAG GGG CCA TCC 3'  
Destroys Apa I site



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## Figure 17a

Frame 1 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser  
ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG GTC TTG TCC  
9 18 27 36 45 54

+1  
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr  
CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC ACC  
66 75 84 93 102 111 120

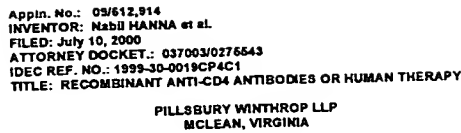
Cys Ser Val Ser Gly Gly Ser Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro  
TGC AGT GTC TCT GGT GGC TCC ATC AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA  
129 138 147 156 165 174 183

Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr Asn Pro  
GGG AAG GGA CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC AAT CCC  
192 201 210 219 228 237 246

Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys Asn Leu Phe Ser Leu Lys Leu  
TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG AAC CTC TTC TCC CTG AAA CTG  
255 264 273 282 291 300 309

Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu  
AGG TCT GTG ACC GCC GCG GAC ACG GCC GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT  
318 327 336 345 354 363 372

His Trp Leu Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
CAC TGG TTA TTA TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG GGG  
381 390 399 408 417 426 435



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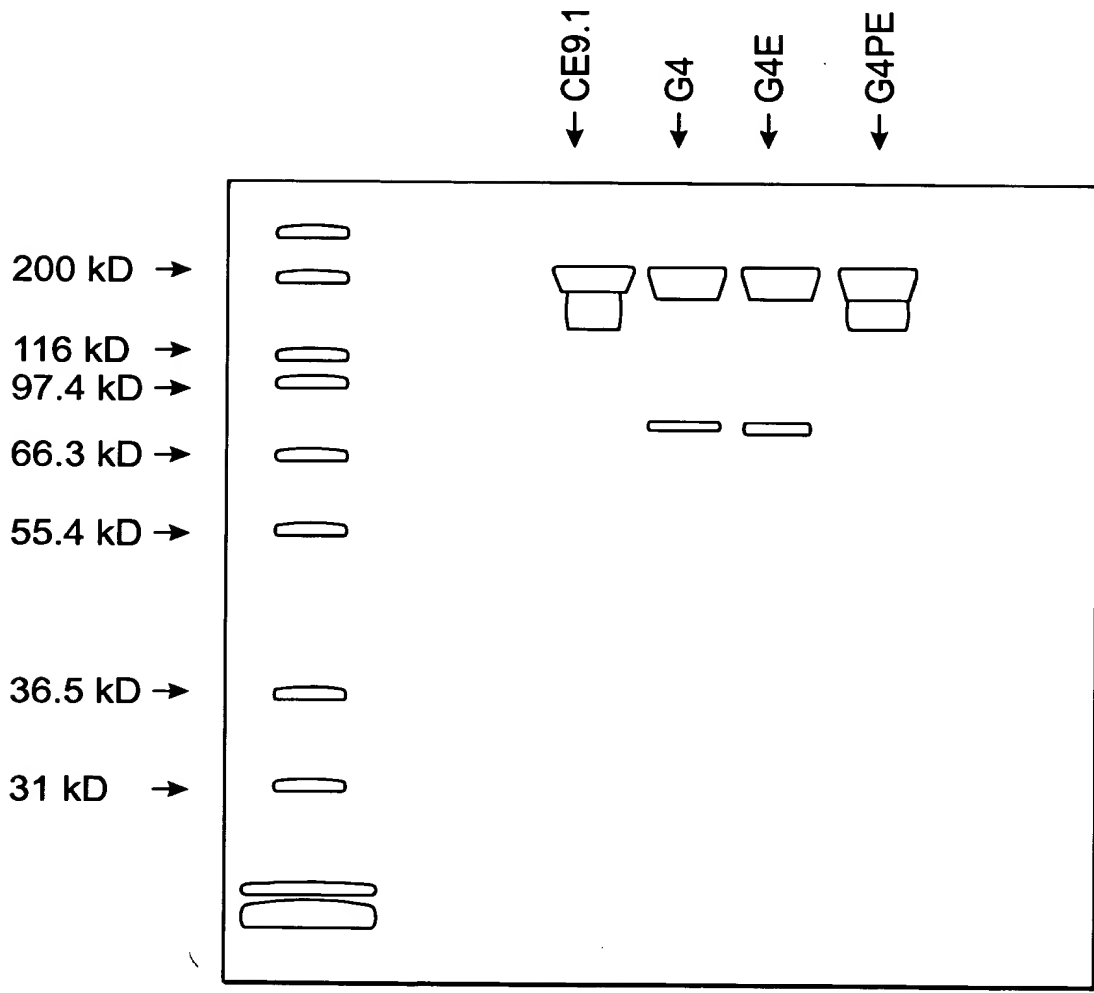


Figure 18

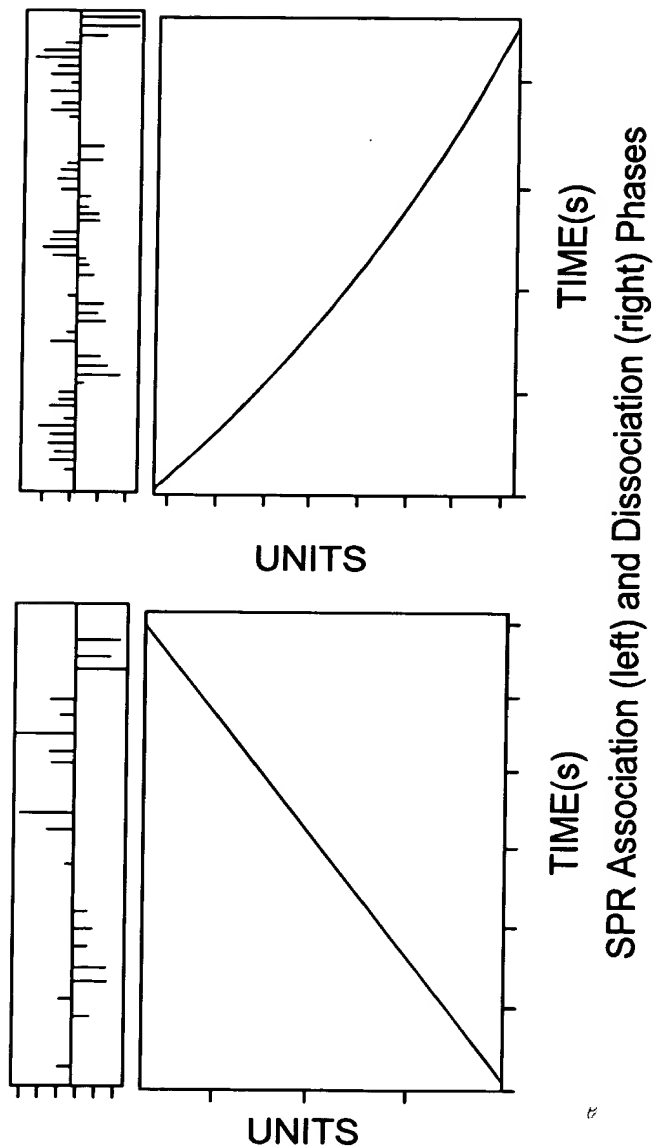


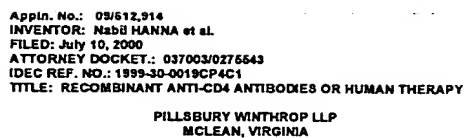
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Figure 19





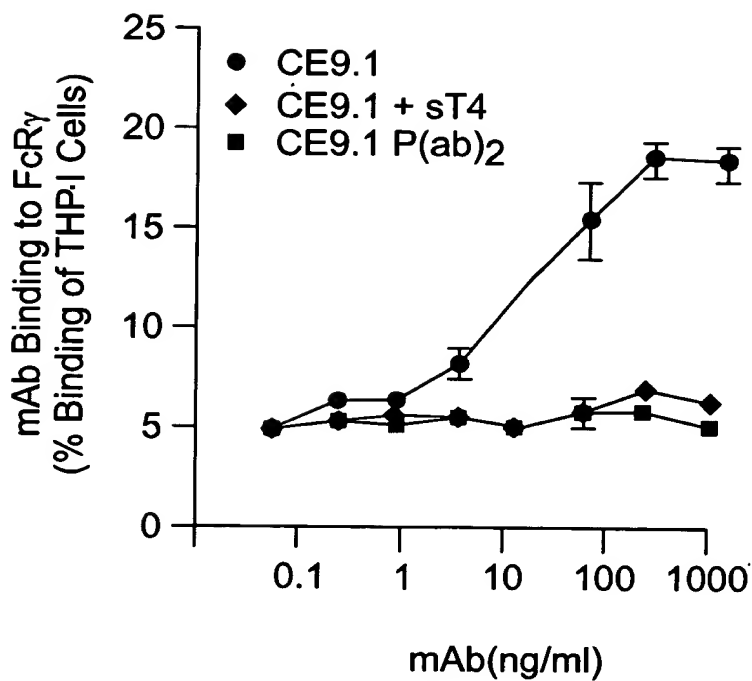


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Figure 21

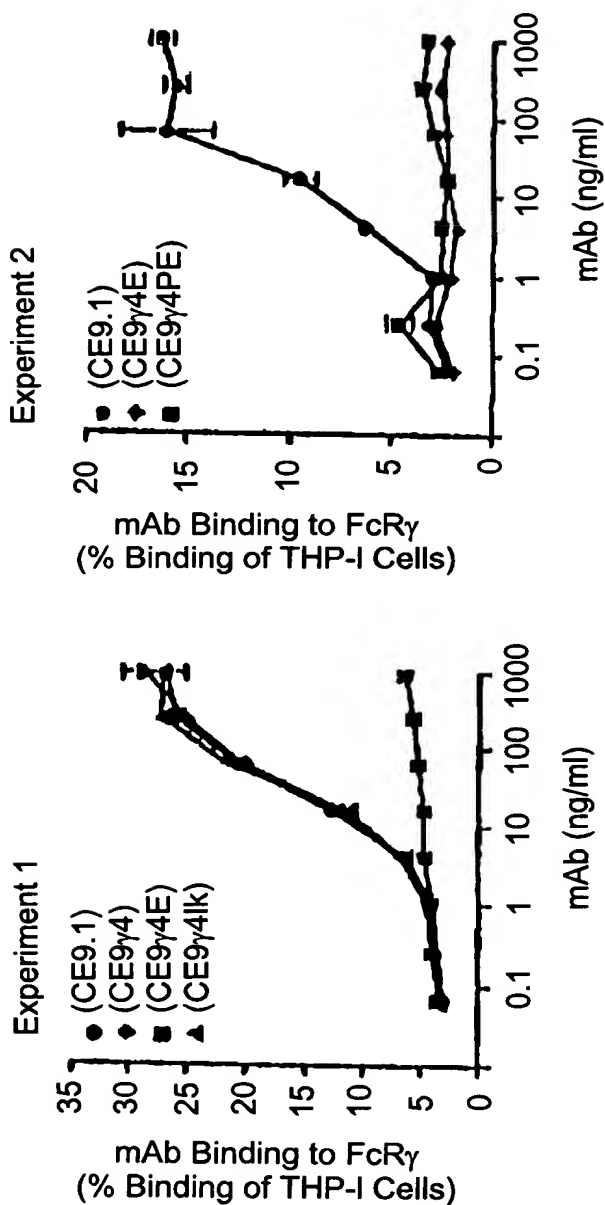




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Figure 22





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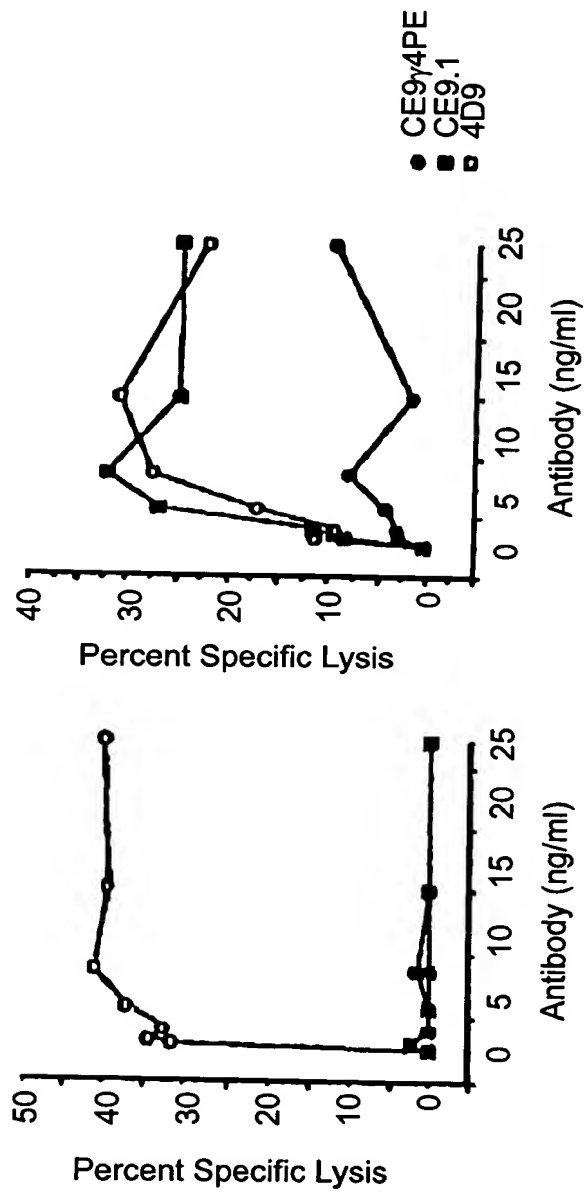
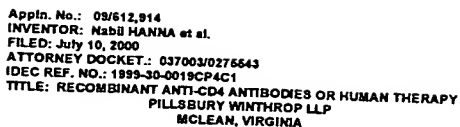


Figure 23



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Figure 1 is a semi-logarithmic plot showing the plasma concentration (ug/ml) of diazepam versus time (Hour) for eight rats. The y-axis is logarithmic, ranging from 0.01 to 100 ug/ml. The x-axis is linear, ranging from 0 to 700 hours. The rats are grouped into two pairs: E (Epileptic) and PE (Post-Epileptic). The legend identifies the rats by their symbols: E, rat # 15 (open square), E, rat # 16 (open triangle), E, rat # 17 (asterisk), E, rat # 18 (open circle), PE, rat # 13 (open square), PE, rat # 14 (open triangle), PE, rat # 19 (open circle), and PE, rat # 20 (asterisk). The plot shows that plasma concentrations generally decrease over time for all rats, with the PE rats showing a more rapid decline than the E rats.



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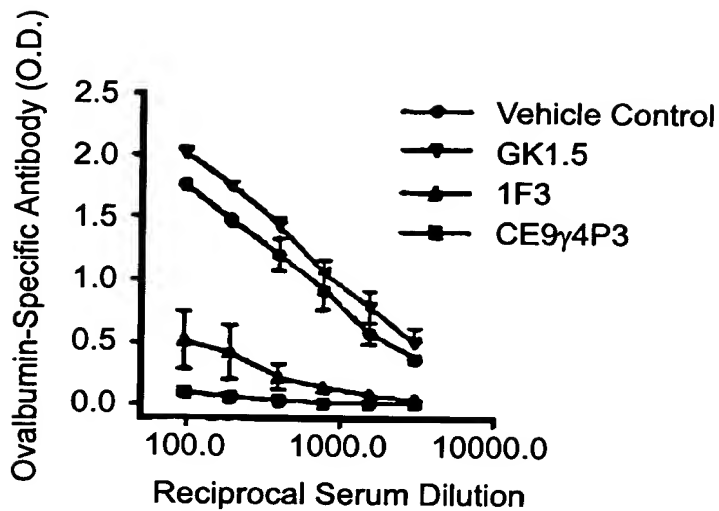


Figure 25